

FIG. 1A

SEQ ID NO: 6 A33 186 . . . P L A Q P A S G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T Q F C N I T V
SEQ ID NO: 1 40628 184 S H S S Y V L H P T T G E L V F D P L S A S D T G E Y S C E A R N G Y G T P M T S N A V
SEQ ID NO: 2 45416 188 I K V A T L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F V V K D
SEQ ID NO: 9 35638 186 T N S S Y T M N T K T G T L Q F N T V S K L D T G E Y S C E A R N S V G Y R R C P G K R
SEQ ID NO: 10 JAM 184 M N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A

A33 227 A V R S P S M N V A L Y V G I A V G V V A A L I I I G I I I Y C C C C R G K D D N T E D K E D A . .
40628 228 R M E A V E R N V G V I V A A Y L V T L L L G I L V F G I W F A Y S R G H F D R T K K G T S . . .
45416 233 S S K L L K T K T E A P T T M T Y P L K A T S T Y K Q S W D W T T D M D G Y L G E T S A G P G K S L
35638 230 . M Q V D D L N I S G I I A A Y V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S . .
JAM 228 H M O A V E L N V G G I V A A Y L V T L L L G L L I F G V W F A Y S R G Y F E T T K K G T A P . .

A33 275 . R P N R E A Y E E P P E Q L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
40628 275 S K K V I Y S Q P S A R S E G E F K Q T S S F L V
45416 283 P V F A I I L I I S L C C M V V F T M A Y I M L C R K T S Q Q E H V Y E A R
35638 277 . N S S S K A T T M . S E N V Q W L T P V I P A L W K A A A G G S R G Q E F
JAM 276 G K K V I Y S Q P S T R S E G E F K Q T S S F L V

FIG. 1B

SEQ ID NO:1

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Met Gly Thr Lys Ala Gln Val Glu Arg Lys Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Gys Ser Leu Ala Leu Gly Ser Val Thr
1      5      10      15      20      25      30
val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val
35      40      45      50      55      60
Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu
65      70      75      80      85      90
Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly
95      100      105      110      115      120
Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
125      130      135      140      145      150
Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
155      160      165      170      175      180
Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
185      190      195      200      205      210
Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
215      220      225      230      235      240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
245      250      255      260      265      270
Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
275      280      285      290      295      299

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FIG._2

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SEQ ID NO:2
 1 MGILLGLLLL GHLTVDITYGR PILEVPESVT GPWKGDVNL P CTYDPLQGYT QVLVKWLVQR GSDPVTIFLR DSSGDHIQQA KYQGRLVHSH KVPGDVSLQL
 101 STLEMDDRSH YTCEVTWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTCGSG YGFTVPQGM R ISLQCQARG S PPISYIWKQ QTNQEPKIV ATLSTLLFKP
 ^Glycosaminoglycan attachment site
 201 AVIADSGSYF CTAKQVGSE QHSDIVKFV KDSSKLLKTK TEAPTTMTYP LKATSTVKQS WDWTDM DGY LGETSAGPGK SLPVFAILLI ISLCCMVVFT
 ^Transmembrane domain

FIG._3

301 MAYIMLCRKT SQEHVYEAA R

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OLI2162 (35936.f1)
 SEQ ID NO:12
 TCGCGGAGCTGTGTTCTGTTTCCC
 OLI2163 (35936.p1)
 SEQ ID NO:13
 TGATCGCGATGGGACAAAGGCGCAAGCTCGAGAGGAACTGTTGTGCCT
 OLI2164 (35936.f2)
 SEQ ID NO:14
 ACACCTGGTTCAAAGATGGG
 OLI2165 (35936.r1)
 SEQ ID NO:15
 TAGGAAGAGTTGCTGAAGGCACGG
 OLI2166 (35936.f3)
 SEQ ID NO:16
 TTGCCTTACTCAGGTGCTAC
 OLI2167 (35936.r2)
 SEQ ID NO:17
 ACTCAGCAGTGTAGGAAAG

FIG._8

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DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100
GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
AACAAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
TGTCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

FIG._4A

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
GCGCAAGCTC GAGAGGAAAC TGTGTGCCT CTTCATATTG GCGATCCTGT 150
TGTGCTCCCT GGCATTGGGC AGTGTTACAG TTGCACTCTT CTGAACCTGA 200
AGTCAGAAAT CCTGAGAATA ATCCTGTGAA GTTGTCTGT GCCTACTCGG 250
GCTTTTCTTC TCCCCGTGTG GAGTGGAAGT TTGACCAAGG AGACACCACC 300
AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAGACA 400
CTGGGACATA CACTTGATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500
TAACATCCCC TCCTCTGCCA CCATTGGGAA CCGGGCAGTG CTGACATGCT 550
CAGAACAAGA TGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTTGAT CCCCTGTCAG 700
CCTCTGATAC TGGAGAATAC AGCTGT 726

FIG._4B

consen02 SEQ ID NO:5

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
TAAGATTACT GAGCTCCGTG TCCAGAACT CTCTGTCTCC AAGCCCACAG 200
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT 400
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTG TG 650
CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAATA CTCTGATGAG 850
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
AGGGCAAAAG TGTCTGTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC 1000
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100
GGGAGTCACT GGCTTTGCCC TGGAATTTGC CAGATGCATC TCAAGTAAGC 1150
CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG 1300
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT 1400
TATTTACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
AAA 1503

FIG._4C

SEQ ID NO:11 GGAGTCCTT CGCGGGCTGT TGTGTAGTG GCCTGATCGC GATGGGGACA AAGGGGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT 100
TGGCGATCCT GTTGTGCTCC CTGGCATTTGG GCAGTGTTAC AGTGCACTCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AATCCTGTGA AGTTGTCCTG 200
TGCCTACTCG GGCTTTCTT CTCCCGGTGT GGAGTGGAG TTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCCTAT 300
GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC ACGGGAAGAC ACTGGGACAT ACACCTGTAT GGTCTCTGAG GAAGGCGGCA 400
ACAGCTATGG GGAGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC CTCTCTGCC ACCATTGGGA ACCGGGCAGT 500
GCTGACATGC TCAGACAAAG ATGGTTCCCC ACCTTCTGAA TACACCTGGT TCAAGATGG GATAGTATG CCTACGAATC CCAAAAGCAC CCGTGCCTTC 600
AGCAACTCTT CCTATGTCTT GAATCCACCA ACAGGAGAGC TGGTCTTTGA TCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700
GGTATGGGAC ACCCATGACT TCAATGCTG TGCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAAACC TGATTCTCCT 800
GGGAATCTTG GTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA GAAAGGACT TCGAGTAAGA AGGTGATTA CAGCCAGCCT 900
AGTGCCCGAA GTGAAGGAGA ATTCAAAACAG ACCTCGTCAAT TCCTGGTGTG AGCTGGTGG GCTCACCACC TATCATCTGC ATTTGCCCTTA CTCAGGTGCT 1000
ACCGGACTCT GGCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTTGT CTCTACACC CCACAGGGCC CCTACTTCT TCGGATGTGT TTTTAATAAT 1100
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAAT TGTTTAAAGT GTTTATTCCT CATTCTTTG 1200
AGGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGCGGGGGT CGCAGGAATC TGCACCTCAAC TGCCACCTG 1300
GCTGGCAGGG ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTTT TGGTGTGAC TGACGACCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400
CTAGAGCGGC TGAATGGTT GTTGGTGTAT GACACTGGGG TCCTTCCATC TCTGGGGCCC ACTCTCTTCT GTCTTCCAT GGGAAGTGCC ACTGGGATCC 1500
CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTCTGTGT GGAAATGGG AGCTCTTGT GTGGAGAGCA TAGTAAATTT TCAGAGAACT 1600
TGAAGCCAAA AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGGGCA GTGGCTCAG CCTGTAATCC CAGAGGCTGA GGCAGGCGGA 1700
TCACCTGAGG TCGGGAGTC GGGATCAGCC TGACCACACAT GGAGAACCC TACTGGAAAT ACAAAGTTAG CCAGGCATGG TGGTGCAATG CTGTAGTCCC 1800
AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

FIG.-5

SEQ ID NO:7

1 CCCACGGCT CGCCACGGC TCCGCCACG GGTCCGCCCA CGCGTCCGG CCACCAAGAG TTTCAGCCTC TTTCGTAGCA GGAGGTGGA AGAAGGACA
GGGTGGCAG CGGGGTGGC AGGGGGTGC CCAGGGGGT CCAGGGGGT GGTGCTCTTC AACTCGGAG AAACCATCGT CCTCCGACCT TCTTCTCTGT

101 GAAGTAGCTC TGGCTGTGAT GGGGATCTTA CTGGGCTGCC TACTCTCTGG GCACCTAACA GTGCACACTT ATGCCCGTCC CATCCTGGA GTGCCAGACA
CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGAGG ATGAGGACCC CGTGCAATTGT CACTGTGAA TACCGGCAGG GTAGGACCTT CACGGTCTCT

1 SEQ ID NO:2 M G I L L G L L L G L L G H L T V D T Y G R P I L E V P E S
*MET

201 CTGTAACAGG ACCTTGGA A GGGGATGTA ATCTTCCCTG CACCTATGAC CCCCTGCCAG GCTACACCCA AGTCTTGGT AAGTGGCTGG TACAACGTGG
CACATTGTCC TGGAACTTT CCCCTACACT TAGAAGGAC GTGGATACTG GGGGACCTTC CGATGTGGT TCAGAACCAC TTCACCGACC ATGTTGCACC

29 V T G P W K G D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCAGACCC CTACCATCT TTCTACGTA CTCTTCTGGA GACCATATCC AGCAGGCAA GTACCAGGC CGCTGCATG TCAGCCACAA GGTTCACGGA
GAGTCTGGA CAGTGGTAGA AAGATGCACT GAGAAGACT CTGGTATAGG TCCTCGCTTT CATGTCCCG GCGACGTAC ACTCGGTGTT CCAAGGTCT

62 S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G

401 GATGTATCCC TCCAATTGAG CACCCTGGAG ATGGATGACC GGAGCCACTA CAGCTGTGAA GTCACTGGC AGACTCCTGA TGGCAACCAA GTCGTGAGAG
CTACATAGG AGGTAACTC GTGGGACCTC TACCTACTGG CCTCGGTGAT GTGCACACTT CAGTCGACCG TCTGAGGACT ACCGTGGTT CAGCACTCTC

95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATAAGATTAC TGACCTCCGT GTCCAGAAAC TCTCTGTCTC CAAGCCCA GTCACAACTG GCAGCGGTTA TGGCTTCAGG GTGCCCCCAG GAATGAGGAT
TATTCTAATG ACTCGAGGCA CAGGTCTTTG AGAGACAGAG GTTCGGGTGT CACTGTTGAC CGTCGCCAAT ACCGAAGTGC CACGGGTCC CTTACTCTCA

129 K I T E L R V Q K L S V S K P T V T T G S G Y G F T V P Q G H R I

601 TAGCCTTCAA TGGCAGGCTC GGGGTTCTCC TCCCATCAGT TATATTTGGT ATAAGCAACA GACTAATAAC CAGGAACCCA TCAAAGTAGC AACCTAAGT
ATCGGAAGTT ACGGTCCGAG CCCCAGAGG AGGGTAGTCA ATATAAACCA TATTCTGTGT CTGATTATTG GTCTTGGGT AGTTTCATCG TTGGGATTCA

162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

FIG._6A

SEQ ID NO:7 701 ACCTTACTCT TCAAGCCTGC GGTGATAGCC GACTCAGGCT CCTATTCTCT CACTGCCAAG GCCAGGTTG GCTCTGACCA GCACAGGCAC ATTGTCAAGT
TGGAAATGAGA AGTTCCGACG CCACTATCGG CTCAGTCCGA GGATAAGAC GTGACGGTTC CCGTCCCAAC CGAGACTCGT CGTGTGCGTG TAACTACTCA
SEQ ID NO:2 195 T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F

801 TTGTGGTCAA AGACTCCTCA AAGCTACTCA AGACCAAGAC TGAGGCACCT ACAACCATGA CATACCCCTT GAAAGCAACA TCTACAGTGA AGCAGTCTCTG
AACACCACTT TCTCAGGAGT TTCGATGAGT TCTGGTTCTG ACTCCGTGGA TGTGGTACT GTATGGGAA CTTTCTGTTGT AGATGTCACT TCGTCAGGAC
229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W

901 GGA CTGGACC ACTGACATGG ATGGCTACCT TGGAGAGACC AGTCTGGG CAGGAAAGAG CCTGCCCTCTC TTTGCCATCA TCCTCATCAT CTCCTTGTGC
CCTGACTGG TGA CTGTACC TACCGATGGA ACCTCTCTGG TCACGACCCG GTCCTTTCTC GGACGGACAG AACGGTAGT AGGACTAGTA GAGGAACACG
262 D W T T D M D G Y L G E T S A G P G K S L P V F A I I L I I S L C

1001 TGTATGGTGG TTTTACCAT GGCTATATC ATGCTCTGTC GGAGACATC CCACACAGAG CATGCTTAGG AAGCAGCCAG GTAAGAAAGT CTCCTCTCTT
ACATACCACC AAAAATGGTA CCGGATATAG TACGAGACAG CTTTCTGTAG GTTGTTCTC GTACAGATGC TTCTGTCGTC CATTCCTTCA GAGAGGAGAA
295 C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGA CCCCCTCCCT GCCCTCAAT TTGATTACTG GCAGGAATG TGGAGGAAG GGGGTGTGC ACAGACCCAA TCCTAAGGCC GGAGGCCCTT
GGTAAAACT GGGGCAGGA CCGGAGTTAA AACTAATGAC GGTCTTTAC ACCTCCTTCC CCCACACCG TGTCTGGTT AGGATTCCGG CCTCCGGAAG

1201 AGGCTCAGGA CATAGCTGCC TTCCCTCTCT CAGGCACCT CTGAGTTGT TTTGGCCCTC TGAACACAAA GGATAATTTA GATCCATCTG CCTTCTGCTT
TCCCAGTCT GTATCAGCG AAGGAGAGA GTCCGTGGA GACTCCAACA AAACCGGGAG ACTTGTGTTT CCTATTAAAT CTAGGTAGAC GGAAGACGAA

1301 CCAGAAATCC TGGGTGGTAG GATCCTGATA ATTAATTGCC AAGATTGAG GCAGNAGGT GGGAAACCAG GACCACAGCC CCACTCCCT TCTTATGGGT
GGTCTTAGG ACCCACCATC CTAGGACTAT TAATTAACCG TTCTTAATC CGTCTTCCA CCCTTTGGTC CTGCTGTCGG GGTTCAGGGA AGAATACCCA

1401 GGTGGGTCT TGGGCCATAG GGCACATGCC AGAGAGGCCA ACCACTCTGG AGAAACCATG AGGGTGGCCA TCTTCCCAAG TGGTGTCTCC AGTGATCAGC
CCACCCGAGA ACCCGGTATC CCGTGTACCG TCCTCCGGT TCTGTAGACC TCTTTGGTAC TCCCACCCGT AGAAGGCTC ACCGACGAGG TCACTACTCG

1501 CAACTTCCCA GAATCTGGG AACAACTACT CTGATGAGCC CTGCATAGGA CAGGAGTACC AGATCATGCC CCAGATCAAT GGCAACTAGC CCGCCCTGCT
GTTGAAGGT CTTAGACCCG TTGTTGATGA GACTACTCG GACGTATCCT GTCTCATCG TCTAGTAGCG GGTCTAGTTA CCGTTGATGC GCGCGGACGA

FIG._6B

SEQ ID NO:7

1601 GGACACAGTT CCTCTGGATT ATGAGTTTCT GGCACATGAG GGCAAAAGTG TCTGTTAAA ATGCCCCATT AGCCAGGAT CTGCTGACAT AATTGCCTAG
CCTGTGTCAA GGAGACCTAA TACTCAAAGA CCGGTGACTC CCGTTTTCAC AGACAATTTT TACGGGGTAA TCCGGTCTTA GACGACTGTA TTAACGGATC

1701 TCAGTCCCTG CCTTCTGCAT GGCCTTCTTC CCTGCTACCT CTCCTCCCTG ATAGCCCAA GTCTCCGCT ACCAACACTG GAGCCGCTGG GAGTCACTGG
AGTCAGGAAC GGAAGACCTA CCGGAAGAAG GGACGATGGA GAGAAGGACC TATCGGGTTT CACAGGCGGA TGCTTGTGAC CTCGGCGACC CTCAGTGACC

1801 CTTTGCCCTG GAATTGCGA GATGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GCCTTCTAG TATCTCTGCC GGGGGCTTCT GGTACTCTCTC
GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCATTCCGT CGACGACCTA AACCAGACC CGGAAGATC ATAGAGACGG CCCCCGAAGA CCATGAGGAG

1901 TCTAAATACC AGAGGGAAGA TGCCCATAGC ACTAGGACTT GGTCAATCATG CCTACAGACA CTATTCNACT TTGGCATCTT GCCACCAGAA GACCCGAGGG
AGATTTATGG TCTCCCTTCT ACGGGTATCG TGATCCTGNA CCAGTAGTAC GGATCTCTGT GATAGTTGA AACCGTAGAA CCGTGGTCTT CTGGGCTCCC

2001 AGGCTCAGCT CTGCCAGCTC AGAGGACCAG CTATATCCAG GATCAATTTCT CTTTCTTCAG GGCAGACAG CTTTAAATG AAATTGTTAT TTCACAGGCC
TCCGAGTCCA GACGGTCGAG TCTCCTGGTC GATATAGGTC CTAGTAAAGA GAAAGAAAGTC CCGCTCTGTC GAAATTAAC TTTAACAAATA AAGTGTCCGG

2101 AGGGTTCACT TCTGCTCCTC CACTATAAGT CTAAATGTTCT GACTCTCTCC TGGTGTCTCA TAAATATCTA ATCATAACAG C
TCCCAAGTCA AGACGAGGAG GTGATATTCA GATTACAGCA CTGAGAGAGG ACCACGAGT ATTATATAGAT TAGTATTGTC G

FIG._6C

SEQ ID NO:8

CCGAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCT
CAGAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGCAGGAGCCGCCACCGCCTCCTCCT
GCTGCTGCTGCGCTACCTGGTGGTGC CCCTGGGCTATCATAAGGCCTATGGGTTTTCTGC
CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA
AACCCCAAAGAAGACTGTTTCTCCTCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTC
CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA
TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT
TAGTGCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT
AGTG GCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGA ACTGTGGT
AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGA
TGGCATCCGTTTGCTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAC
AATGAATACAAAACTGGA ACTCTGCAATTTAATACTGTTTCCAACTGGACACTGGAGA
ATATTCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT
TTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC
CTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGTGCAGTG
GCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGCGGGCGGATCACGAGGTCAGGA
GTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATACAAAAATTAG
CTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTTGGGAGACAGGAGAATCACTTGA
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGGTAA
CAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATACTGGTTTTTACC
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIG. 7

SEQ ID NO:9

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSC EVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNI
SGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMS ENVQWLTPV
IPALW KAAAGGSRGOEF

FIG. 11

SEQ ID NO:5

1 GCAGGCAAG TACCAGGGCC GCCTGCATGT GACCCACNAG GTTCCAGGAG ATGTATCCCT CCAATTGACC ACCCTGGAGA TGATGACCG GAGCCACTAC
 CGTCCGTTT ATGCTCCCG CGGACGTACA CTCGGTGTTT CAAGTCTCT TACATAGGGA GGTAACTCG TGGGACCTCT ACCTACTGGC CTCGGTGATG
 ^42257.f1 SEQ ID NO:18 ^42257.p1 SEQ ID NO:22

101 ACGTGTGAAG TCACCTGGCA GACTCCTCAT GGCNACCAAG TCGTGAGAGA TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCACAG
TGCACACTTC AGTGGACCGT CTGAGGACTA CCGTGTGTTT AGCACTCTCT ATTCTAATGA CTCGAGGCAC AGGTCTTTGA GAGACAGAGG TTCCGGGTGC

201 TGACAACTGG CAGCGGTAT GGTTCACGG TCGCCACAGG AATGAGGATT AGCCTTCAAT GCCAGGCTTC GGGGTTCTCC TCCCATCAGT TATATTGGT
 ACTGTTGACC GTCGCCAATA CCGNAGTGCC ACGGGGTCCC TTACTCCTAA TCGGAAGTTA CCGTCCCAAG CCCCAGAGG AGGTAGTCA ATATAACCA

301 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAGTAG CAACCCTAAG TACCTTACTC TTCNAGCCCTG CCGTGATAGC CGACTCAGGC TCCTATTCT
 TATTGGTGT CTGATTATTG GTCCCTTGG GTCTTTCATC GTTGGGATTG ATGGAATGAG AAGTTCGGAC GCCACTATCG GCTGAGTCCG AGGATAAAGA

401 GCACTGCCAA GGGCCAGTT GGCTCTGACC AGCAGAGCGA CATGTGTAAG TTTGTGCTCA AAGACTCCTC AAGACTACTC AAGACCAAGA CTGAGGCACC
CGTGACGGTT CCCGGTCCAA CCGAGACTCG TCGTGTGCTT GTAACACTTC ^42257.f1 SEQ ID NO:20 ^42257.f2 SEQ ID NO:19

501 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTCTCTGG
 ATGTTGGTAC TGTATGGGA ACTTTCGTTG TAGATCTCAC TTCTCAGGA CCGTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCAGGACCC

601 CCAGGAAAGA GCCTGCCCTGT CTTTGGCATC ATCCTCATCA TCTCCTTGTG CTGTATGCTG GTTTTACC TGGCCTATAT CATGCTCTGT CCGAAGACAT
 GGTCTTTCT CGGACGGACA GAAACGGTAG TAGGACTAGT AGAGGAACAC GACATACCAC CAAAATGCT ACCGGATATA GTACGAGACA GCCTTCTGTA
 ^42257.f2 SEQ ID NO:19

701 CCCAACAGA GCATGTCTAC GAAGCAGCCA GGGACATGC CAGAGAGGCC AAGCACTCTG GAGAAACCAT GAGGTGGCC ATCTTCCAA GTGGCTGCTC
 GGGTGTCTT CGTACAGATG CTTCTGTCGT CCCGTGACG GTCTCTCCG TTGCTGAGAC CTCTTTGGTA CTCCCACCG TAGAAGCGTT CACCGACGAG

FIG._9A

SEQ ID NO:5

801 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCACAACTA CTCTGATGAG CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA
GTCACTACTC GGTGAGGG TCTTAGACCC CGTTGTTGAT GAGACTACTC GGGACGTATC CTGTCTCTCAT GGTCTAGTAG CCGGTCTACT TACCGTTGAT

901 CGCCCGCCCTG CTGGACACAG TTCTCTCTGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGTCTGTTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC
GCGGCGGAC GACCTGTGTC AAGGAGACCT AATACTCAAA GACCGGTGAC TCCCGTTTTC ACACACAATT TTACGGGGT AATCCGGTCC TAGACGACTG

1001 ATAAATGCCT ACTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC CTCTCTTCTT GGTAGCCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT
TATTAACGGA TCAGTCAGGA ACGGAAGACG TACCGGAAGA AGGACGATG GAGAGAAAGGA CCTATCGGGT TTCACAGCGG GATGGTTGTG ACCTCGGGCA

1101 GGGAGTCACT GCGTTTGCCC TGGAAATTGC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT
CCCTCAGTGA CCGAAACGGG ACCTTAACG GTCTACGTAG AGTTCATTCTG GTGACGACGACC TAAACCGAGA CCGGGGAAGA TCATAGAGAC GGGCCCCGAA
^42257.r2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCCATG GCACCTAGGAC TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG
GACCATGAGG AGAGATTAT GGTCTCCCTT CTACCGGTAT CCGTATCCTG AACCATGACT ACGGATCTCT GTGATAAGTT GAAACCGTAG AACGGTGGTC

1301 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC CAGGATCAAT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT
TTCTGGGCTC CCCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCCATATAG GTCCATAGTAA AGAGAAAGAA GTCCCGGTCT GTCGAAAATT AACTTTAACA

1401 TATTTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT TCTGACTCTC TCCTGGTCT CAATAAATAT CTAATCATAA CAGCAAAAAA
ATAAAGTGTG CCGTCCCAAG TCAAGACGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCACGA GTTATTATATA GATTAGTATT CTCGTTTTTT

1501 AAA
TTT

FIG._9B

A33 HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS). EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPR---VEW-KFDQGDTRLVC--YNN
SEQ ID NO:23

SEQ ID NO:23
 A33_human
 SEQ ID NO:24

DNA40628 283 K--ITAS-YEDRVTFI-----PTGITFKSVTREDTGTYTCMVS---EEGGNSYGEVKKVK
 * * * * * . * * * * * . * * * * *
 A33 human 77 KNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYESVLSMSDLEGNT--KSRVR

DNA40628 427 LVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIWPTNPKSTRAFSN
 *.***** * *** *** .***. *. *
 A33 human 135 LVLVPPSKPEGIEGTIIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP-----

DNA40628 607 SSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPTMTSNAVRMEAVERNVG- --IVA
A33 human 187 ---LAQPASGQPVSLKNISTDTSGYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIAV

DNA40628 775 AVLVTLLILGILVFGIWFAYSRGHFDRT--KKGTSKKVIYSQP
* . **..*.*... ** * * * . * . *
A33 human 244 GVVAALIIIGIIYY--CCCCRGKDDNTEDKEDARPNREAYEEP

FIG. 10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19
IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1

DNA40628 112 LC SL--ALGSVTVHSSEPEVRIPENNPVKLSA YSGFSSPR---VEW-KFDQGD TTRLVC
SEQ ID NO:25

A33 human 12 LCAVRVTVD AISVETPQDVL RASQKSVTL PCTYHTSTSSREGLIQWDKLL LTHTERVVI
SEQ ID NO:26

DNA40628 274 --YNNK--ITAS-YEDRVTF L-----PTGITFKSVTREDTGTYTCMVSEEGGNSYGEVK
A33_human 72 WPF SNKNIYIHGELYKNRVSI SNNAEQDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA40628 421 --VKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGI VMP TNP KSTR
A33_human 131 SRVRL LVLVPPSKPECGIEGETIIGNNIQLTCQSKESPTPQYSWKRYN ILNQEQP----

DNA40628 595 AFSNSSYVLNP TTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAV RMEAVERNVGV--
A33_human 187 -----LAQPASGQPVSLKNISTDTSGYICTSSNEEGTQFCNITVA VRSPSMNVALYV

DNA40628 766 -IVA AVLVT LILLGILVFGIWFAYS RGHFDRT--KKGTS SKKVIYSQP
A33_human 240 GIAVG VVAALIIIGIIY---CCCCRGKDDNTEDKEDARPNREAYEEP

FIG._10B

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SEQ ID NO: 6  A33_hum  1  . . . . . M V G K M W P V L W T L C A V R V T V D A I S V E T P O O V L R A S Q G K S V T L
SEQ ID NO: 1  40628  1  M G T K A Q V E R K L L C L F I A I L L C S . . L A L G S V T V H S S E P E V R I P E N N P V K L

A33_hum      42  P C T Y H T S T S S R E G L I O W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I
40628        49  S C A Y S G F S S P R . . . V E W . K F D Q G D T T R L V C . . Y N N K . . I T A S . Y E D R V T F

A33_hum      92  S N N A E Q S D A S I T I D O L T M A D N G T Y E C S V S L M S D L E G N T K S R V R L L V L V P P
40628        90  . . . . . L P T G I T F K S V T R E D T G T Y T C H V S E E G G . N S Y G E V K V K L I V L V P P

A33_hum     142  S K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N O E Q P . . . . .
40628     133  S K P T V N I P S S A T I G N R A V L T C S E Q D G S P S E Y T W F K D G I V M P T N P K S T R A

A33_hum     187  . . . . . L A Q P A S G Q P V S L K N I S T D T S G Y I C T S S N E E G T Q F C N I T V A V R S
40628     183  F S N S S Y V L N P T T G E . L V F D P L S A S D T G E Y S C E A R N G Y G T P M T S N A V R M E A

A33_hum     231  P S M N V A L Y V G I A V G V V A A L I I G I I I Y C C . C C R G K D D N T E D K E D A R P N R E
40628     232  V E R N V G V . . . I V A A V L V T L I L L G I L V F G I W F A Y S R G H F D R T K K G T S S K K V

A33_hum     280  A Y E E P P E Q L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
40628     279  I Y S O P S A R S E G E F K Q T S S F L V

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FIG._12

SEQ ID NO: 6	A33_hum	1	M	V	G	K	M	W	P	V	L	W	T	L	C	A	V	R	V	T	V	D	A	I	S	V	E	T	P	Q	D	V	L	R	A	S	Q	G	K	S	V	T	L	P	C	T	Y	H	T	S	T	S		
SEQ ID NO: 2	45416	1	.	M	G	I	L	L	G	L	L	L	G	H	L	T	V	D	T	Y	G	R	P	I	L	E	V	P	E	S	V	T	G	P	W	K	G	.	D	V	N	L	P	C	T	Y	D	P	L	O	G			
	A33_hum	51	S	R	E	G	L	I	Q	W	D	K	L	L	T	H	T	E	R	V	V	I	W	.	P	F	S	N	K	N	Y	I	H	G	E	L	Y	K	N	R	V	S	I	S	N	N	A	E	Q	S	D			
	45416	49	Y	T	Q	V	L	V	K	W	.	.	L	V	Q	R	G	S	D	P	V	T	I	F	L	R	D	S	S	G	D	H	I	Q	Q	A	K	Y	Q	G	R	L	H	V	S	.	S	H	K	V	.	P	G	D
	A33_hum	100	A	S	I	T	I	D	O	L	T	M	A	D	N	G	T	Y	E	C	S	V	S	.	L	M	S	D	L	E	G	N	T	K	S	R	V	R	L	L	V	L	V	P	P	S			
	45416	96	V	S	L	Q	L	S	T	L	E	M	D	O	R	S	H	Y	T	C	E	V	T	W	O	T	P	D	G	N	Q	V	V	R	D	K	I	T	E	L	R	V	Q	K	L	S	V	S	K	P	T	V		
	A33_hum	143	K	P	E	C	G	I	E	G	E	T	I	I	G	N	I	O	L	T	C	Q	S	K	E	G	S	P	T	P	Q	Y	S	W	K	R	Y	N	I	L	N	Q	E	Q	P	L	A	Q	P	A	S			
	45416	146	T	T	G	S	G	Y	G	F	T	V	P	Q	G	M	R	I	S	L	Q	C	Q	A	R	.	G	S	P	I	S	Y	I	W	.	.	Y	K	Q	Q	T	N	N	Q	E	P	I	K	V	A	T			
	A33_hum	193	G	O	P	V	S	L	K	N	I	S	T	D	T	S	G	Y	I	C	T	S	S	N	E	E	G	T	.	Q	F	C	N	I	.	T	V	A	V	R	S	P	S	M	N	V	A	L	Y	V	G			
	45416	193	L	S	T	L	L	F	K	P	A	V	I	A	D	S	G	S	Y	F	C	T	A	K	G	Q	V	G	S	E	Q	H	S	D	I	V	K	F	V	V	K	D	S	S	K	L	L	K	T	K	T	E		
	A33_hum	241	I	A	V	G	V	V	A	A	L	I	I	I	G	I	I	I	Y	C	C	C	C	R	G	K	D	D	N	T	E	D	K	E	D	A	R	P	N	R	E	A	Y	E	E	P	P	E	Q	L	R			
	45416	243	A	P	T	T	M	T	Y	P	L	K	A	T	S	T	V	K	Q	S	W	D	T	T	D	M	D	G	Y	L	G	E	T	S	A	G	P	G	X	S	L	P	V	F	A	I	I	I	S					
	A33_hum	291	L	S	R	E	R	E	E	E	D	D	Y	R	Q	E	E	Q	R	S	T	G	R	E	S	P	D	H	L	D	Q																							
	45416	293	L	C	C	H	V	V	F	T	M	A	Y	I	M	L	C	R	K	T	S	O	Q	E	H	V	Y	E	A	A	R																							

FIG.-13

SEQID NO: 6 A33_hum 1 . . . M V G K M W P V L W T L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C
 SEQID NO: 9 35638 1 M A R R S R H R L L L L L R Y L V V A L G Y H K A Y G F S A P K D Q Q V V T A V E Y O E A I L A C

A33_hum 44 T Y H T S T S S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N
 35638 51 . . . K T P K K T V S S R L E W K K L G R S V S F V Y Y Q O T . L Q G D . F K N R

A33_hum 94 N A E Q S D A S I T I D Q L T M A D N G T Y E C S V S L M S D L E G N . T K S R V R L L V L V P P S
 35638 87 . A E M I D F N I R I K N V T R S D A G K Y R C E V S A P S E Q G O N L E E D T V T L E V L V A P A

A33_hum 143 K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A Q P A S
 35638 136 V P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N P R L G S Q S

A33_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T Q F C N I T V A V . . . R S P S M N V A L Y V
 35638 186 T N S S Y T M N T K T G T L Q F N T . V S K L D T G E Y S C E A R N S V G Y R R C P G K R M O V D D

A33_hum 240 G I A V G V V A A L I I G I I I Y C C . . . C C R G K D D N T E D K E D A R P N R E A Y E E P P E
 35638 235 L N I S G I I A A V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S S K A T T

A33_hum 287 Q L R E L S R . E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
 35638 285 M S E N V Q W L T P V I P A L W K A A A G G S R G Q E F

FIG.-14

SEQ ID NO: 10 jam 1 MGT E G K A G R K L L F L F T - S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L T C
 SEQ ID NO: 1 40628 1 MGT K A Q V E R K L L C L F I L A I L L C S L A L G S V T V H S S E P E V R I P E N N P V K L S C

jam 50 T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S S V T
 40628 51 A Y S G F S S P R V E W K F D Q G D T T R L V C Y N N K I T A S Y E D R V T F L P T G I T F K S V T

jam 100 R K D N G E Y T C M V S E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I G N R A V
 40628 101 R E D T G T Y T C M V S E E G G N S Y G E V K V K L I I V L V P P S K P T V N I P S S A T I G N R A V

jam 150 L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S G D L I F
 40628 151 L T C S E Q D G S P P S E Y T W F K D G I - V M P T N P K S T R A F S N S S Y V L N P T T G E L V F

jam 200 D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L N V G G I V A A V L V T L I L
 40628 200 D P L S A S D T G E Y S C E A R N G Y G T P W T S N A V R M E A V E R N V G V I V A A V L V T L I L

jam 250 L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S O P S T R S E G E F K Q T S S F L
 40628 250 L G I L V F G I W F A Y S R G H F D R T K K G T - S S K K V I Y S O P S A R S E G E F K Q T S S F L

jam 300 V
 40628 299 V

FIG._15

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q S D V Q V P E N E S I K L T
SEQ ID NO: 2 45416 1 M G I L L G L L L L G H L T V D T Y G R P I L E V P E S V T G P W K G D V N L P

jam 49 C T Y S . . . G F S S P R V E W K F V Q G S T T A L V . . . C Y N S Q I T A P Y A D R V T F S .
45416 41 C T Y D P L Q G Y T O V L V K W L V O R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H

jam 90 S S G I T F S S V T R K D N G E Y T C M V . . . S E E G G O N Y G E V S I H L T V L V P P
45416 91 K V P G D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R V Q K L S V

jam 132 S K P T I S V P S . . . S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A
45416 141 S K P T V T T G S G Y G F T V P Q G M R I S L Q C Q A R G S P P I S Y I W Y K Q Q T N . . N Q E P

jam 178 K K T R A F M H S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A
45416 188 I K V A T L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V

jam 228 H . . . M D A V E L N V G G I V A A V L V T L I L L G L L I F G . . . V W F A Y S R G Y F E T T K K
45416 227 K F V V K D S S K L L K T X T E A P T T M T Y P L K A T S T V K Q S W D W T T D M D G Y L G E T S A

jam 272 G T A P G K K V I Y S O P S T R S E G E F K Q T S S F L V
45416 277 G P G K S L P V F A I I L I S L C C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R

+

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V . . . P E N E S I K L
SEQ ID NO: 29 35638 1 . . . M A R R S R H R L L L L R Y L V V A L G Y H K A Y G F S A P K D Q Q V V T A V E Y Q E A I L

jam 48 T C . T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S
35638 49 A C K T P K X T V S S R L E W K K L . G R S V S F V Y Y Q Q T L O G D F K N R A E M I D F N I R I K

jam 97 S V T R K D N G E Y T C M V S . . E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I
35638 98 N V T R S D A G K Y R C E V S A P S E Q G Q N L E E D T V T L E V L V A P A V P S C E V P S S A L S

jam 145 G N R A V L T C S E H D G S P S E Y S W F K D G I S M L T A D A K X T R A F M N S S F T I D P K S
35638 148 G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L . E N P R L G S Q S T N S S Y T M N T K T

jam 195 G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L N V G G I V A A V L
35638 197 G T L Q F N T V S K L D T G E Y S C E A R N S V G . Y R R C P G K R M Q V D D L N I S G I I A A V V

jam 245 V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R S E G E F K Q
35638 246 V V A L V I S V C G L G V C Y A Q R K G Y F . . . S K E T S F Q K S N S S S K A T T M S E N V Q W L

jam 295 T S S F L V
35638 293 T P V I P A L W K A A A G G S R G O E F

FIG._17

+

SEQ ID NO: 6 A33_hum 1 M V G K M W P V L W T . L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T
 SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q S O V Q V P E N E S I K L T C T

A33_hum 45 Y H T S T S S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N N
 jam 51 Y S G F S S P R . . . V E W . K F V O G S T T A L V C . . Y N S Q . . I T A P . Y A D R V T F S S .

A33_hum 95 A E Q S D A S I T I D Q L T M A D N G T Y E C S V S L M S D L E G N T K S R V R L L V L V P P S K P
 jam 91 S G I T F S S V T R K D N G E Y T C M V S E E G G . Q N Y G E V S I H L T V L V P P S K P

A33_hum 145 E C G I E G E T I I G N N I O L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A O P A S G Q
 jam 135 T I S V P S S V T I G N R A V L T C S E H D G S P S E Y S W F K D G I S M L T A D A K K T R A F M

A33_hum 195 P V S L K N I S T D T S G Y I C T S S N E E G T O F C N I T V A V R S P S M N . . . V A L
 jam 185 N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L

A33_hum 238 Y V . G I A V G V V A A L I I I G I I I Y C . . . C C C R G K D D N T E D K E D A R P N R E A Y E E
 jam 235 N V G G I V A A V L V T L I L L G L L I F G V W F A Y S R G Y F E . T T K K G T A P G K K V I Y S Q

A33_hum 284 P P E O L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
 jam 284 P S T R S E G E F K Q T S S F L V

FIG. 18

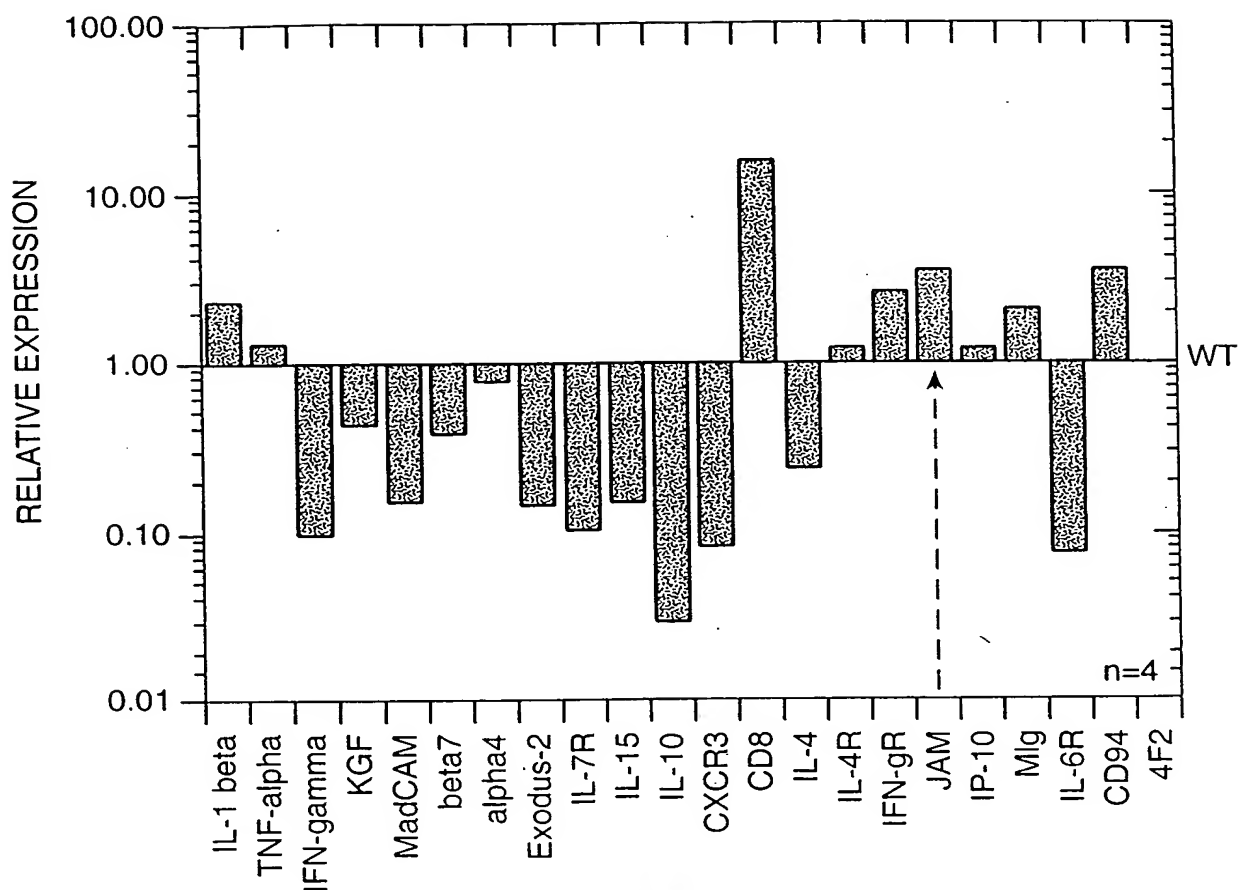
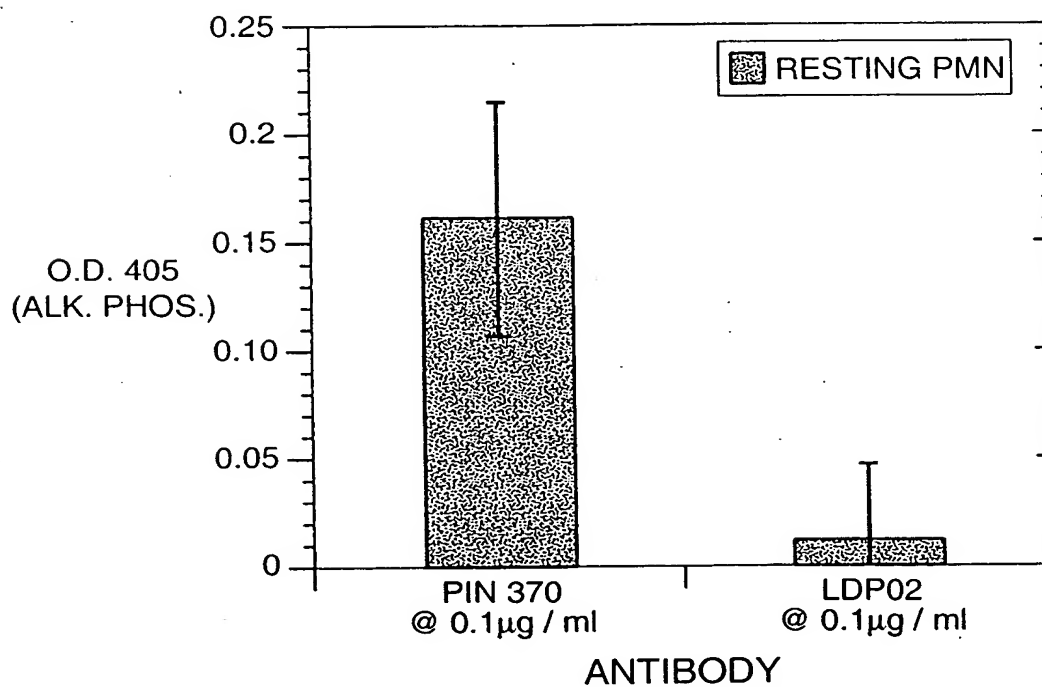
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<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++		
PUTAMEN	+	OVARY	+++	APPENDIX	+
SUSTANTIA NIGRA	+	PANCREAS	++	LUNG	+++
TEMPORAL LOBE	+	PITUITARY GLAND	++	TRACHEA	+++
THALAMUS	+	ADRENAL GLAND	++	PLACENTA	+++
NUCLEUS ACCUMBEUS	+	THYROID GLAND	++		
SPINAL CORD	-	SALIVARY GLAND	+++	FETAL BRAIN	+
		MAMMARY GLAND	++	FETAL HEART	+
				FETAL KIDNEY	++
				FETAL LIVER	+++
				FETAL SPLEEN	+
				FETAL LUNG	+++

FIG. 19



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**FIG. 20****FIG. 21**